



SEQUENCE LISTING

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TECH CENTER 1600/2900

<120> Novel Tumor-Associated Marker

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<170> PatentIn version 3.1

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Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser Asn Ser His Leu Arg  
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Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp Gly  
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Leu Lys Leu Met Leu Leu Leu Glu Phe Ile Ser Gly Glu Arg Leu Pro  
85 90 95

Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val Asn  
100 105 110

Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile Lys Leu Asp Phe His  
115 120 125

Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly Met  
130 135 140

Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu  
145 150 155 160

Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr  
165 170 175

B1  
Cont

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195 200 205

Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu Asn  
210 215 220

Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu  
225 230 235 240

Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala Ile  
245 250 255

Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys  
260 265 270

Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val  
275 280 285

Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp Tyr Glu Lys Leu Ala  
290 295 300

Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp  
305 310 315 320

Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp  
325 330 335

Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys  
340 345 350

Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln Thr Lys Leu Arg Leu  
355 360 365

Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp  
370 375 380

Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu  
385 390 395 400



Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu  
405 410 415

Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp  
420 425 430

Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu  
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Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp  
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Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ser Ala Gln  
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Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg  
485 490 495

Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His  
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Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile  
515 520 525

Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro Ala Ala Pro Phe Asn  
530 535 540

Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val  
545 550 555 560

His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe  
565 570 575

Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu His  
580 585 590

Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser  
595 600 605

Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys  
610 615 620

Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu  
625 630 635 640

Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu His Leu Arg Arg Gln  
645 650 655

Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met  
660 665 670

Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln  
675 680 685

Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro  
690 695 700

Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu  
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Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val  
725 730 735

Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val  
740 745 750

Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln  
755 760 765

Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly  
770 775 780

Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro His Gln Pro Gly Leu  
785 790 795 800

Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu Phe Asn Arg Ile Met  
805 810 815

Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe  
820 825 830

Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln  
835 840 845

Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr  
850 855 860

Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys  
865 870 875 880

Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Gly Val Arg Gly Ala  
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B!  
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Cont

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Cys Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp  
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Glu Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile  
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Ser Gly Glu Arg Leu Pro Lys Pro Glu Arg Gly Lys Met Arg Val His  
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Lys Ile Asn Asn Val Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly  
 85 90 95

Val Lys Leu Val Ser Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala  
 100 105 110

Lys Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile  
 115 120 125

Gln Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu  
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Phe His Ile Ser Trp Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His  
165 170 175

Arg His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp  
180 185 190

Pro Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu  
195 200 205

Asp Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg  
210 215 220

Pro Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala  
225 230 235 240

Phe Ser Gly Ala Gln Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys  
245 250 255

Val Leu Ala Val Asn Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu  
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Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp  
275 280 285

Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys  
290 295 300

Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val  
305 310 315 320

Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys  
325 330 335

Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Asp Lys Met  
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Val Ser Asp Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys  
355 360 365

31  
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Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu  
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Asp His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Trp  
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Thr Asp Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala  
405 410 415

Thr Leu Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu  
420 425 430

Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile  
435 440 445

Ala Gln Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn  
450 455 460

Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu  
465 470 475 480

Thr His Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu  
485 490 495

Ala Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe  
500 505 510

Asn Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile  
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Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln  
530 535 540

Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu  
545 550 555 560

Ala Ile His Lys Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys  
565 570 575

Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn  
580 585 590

B1  
Cont

Ser Lys Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala  
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Leu Leu Glu Glu Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg Arg  
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Gln Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys  
625 630 635 640

Met Glu Glu Ile Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu  
645 650 655

Asp Gln Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr  
660 665 670

Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu  
675 680 685

Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile  
690 695 700

Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn  
705 710 715 720

Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln  
725 730 735

Glu Gln Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp  
740 745 750

His Gly Gly Ala Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile Ser  
755 760 765

Leu Gly Tyr Asp Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn  
770 775 780

Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe  
785 790 795 800

Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr  
805 810 815



Ala Asp Gln Val Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn  
 820 825 830

Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala  
 835 840 845

Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val  
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Pro Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu  
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<213> Human

<400> 12

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 Asp Glu Ile Leu Asp Phe Gly Tyr Pro Gln Asn Ser Glu Thr Gly Ala  
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 Lys Glu Glu Gln Ser Gln Ile Thr Ser Gln Val Thr Gly Gln Ile Gly  
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 Val Leu Glu Ser Val Asn Leu Leu Met Ser Pro Gln Gly Gln Val Leu  
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 195 200 205  
 Met Pro Glu Cys Lys Phe Gly Met Asn Asp Lys Ile Val Ile Glu Lys  
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 Gln Gly Lys Gly Thr Ala Asp Glu Thr Ser Lys Ser Gly Lys Gln Ser  
 225 230 235 240  
 Ile Ala Ile Asp Asp Cys Thr Phe His Gln Cys Val Arg Leu Ser Lys  
 245 250 255

Phe Asp Ser Glu Arg Ser Ile Ser Phe Ile Pro Pro Asp Gly Glu Phe  
 260 265 270

Glu Leu Met Arg Tyr Arg Thr Thr Lys Asp Ile Ile Leu Pro Phe Arg  
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Val Ile Pro Leu Val Arg Glu Val Gly Arg Thr Lys Leu Glu Val Lys  
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Val Val Ile Lys Ser Asn Phe Lys Pro Ser Leu Leu Ala Gln Lys Ile  
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Glu Val Arg Ile Pro Thr Pro Leu Asn Thr Ser Gly Val Gln Val Ile  
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Cys Met Lys Gly Lys Ala Lys Tyr Lys Ala Ser Glu Asn Ala Ile Val  
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Trp Lys Ile Lys Arg Met Ala Gly Met Lys Glu Ser Gln Ile Ser Ala  
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Glu Ile Glu Leu Leu Pro Thr Asn Asp Lys Lys Lys Trp Ala Arg Pro  
 370 375 380

Pro Ile Ser Met Asn Phe Glu Val Pro Phe Ala Pro Ser Gly Leu Lys  
 385 390 395 400

Val Arg Tyr Leu Lys Val Phe Glu Pro Lys Leu Asn Tyr Ser Asp His  
 405 410 415

Asp Val Ile Lys Trp Val Arg Tyr Ile Gly Arg Ser Gly Ile Tyr Glu  
 420 425 430

Thr Arg Cys  
 435

<210> 13

<211> 1764

<212> DNA

<213> Human

B1  
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<400> 13

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ccagggcctt tgggcggagg tgggtcgggg ggccccaaa tgggcttgcc cccccctccc	240
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cgcacgagg ggttcaccaa cgtcaaggag ctgtatggca agattgccga ggccttccgc	360
ctgccaaactg ccgaggtgat gttttgcacc ctgaacaccc acaaagtga catggacaag	420
ctcctggggg gccaaatcgg gctggaggac ttcattctcg cccacgtgaa ggggcagcgc	480
aaggaggtgg aggtgttcaa gtcggaggat gcactcgggc tcaccatcac ggacaacggg	540
gctggctacg cttcatcaa gcgcatcaag gagggcagcg tgatcgacca catccacctc	600
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B1  
Cont.

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 gctgttaaaa aaaaaaaaaa aaaa 1764

<210> 14

<211> 333

<212> PRT

<213> Human

<400> 14

Met Pro Leu Gly Leu Gly Arg Arg Lys Lys Ala Pro Pro Leu Val Glu  
 1 5 10 15

Asn Glu Glu Ala Glu Pro Gly Arg Gly Gly Leu Gly Val Gly Glu Pro  
 20 25 30

Gly Pro Leu Gly Gly Gly Gly Ser Gly Gly Pro Gln Met Gly Leu Pro  
 35 40 45

Pro Pro Pro Pro Ala Leu Arg Pro Arg Leu Val Phe His Thr Gln Leu  
 50 55 60

Ala His Gly Ser Pro Thr Gly Arg Ile Glu Gly Phe Thr Asn Val Lys  
 65 70 75 80

Glu Leu Tyr Gly Lys Ile Ala Glu Ala Phe Arg Leu Pro Thr Ala Glu  
 85 90 95

Val Met Phe Cys Thr Leu Asn Thr His Lys Val Asp Met Asp Lys Leu  
 100 105 110

Leu Gly Gly Gln Ile Gly Leu Glu Asp Phe Ile Phe Ala His Val Lys  
 115 120 125

Gly Gln Arg Lys Glu Val Glu Val Phe Lys Ser Glu Asp Ala Leu Gly  
 130 135 140

Leu Thr Ile Thr Asp Asn Gly Ala Gly Tyr Ala Phe Ile Lys Arg Ile  
 145 150 155 160

B1  
 Cont.

Lys Glu Gly Ser Val Ile Asp His Ile His Leu Ile Ser Val Gly Asp  
 165 170 175

Met Ile Glu Ala Ile Asn Gly Gln Ser Leu Leu Gly Cys Arg His Tyr  
 180 185 190

Glu Val Ala Arg Leu Leu Lys Glu Leu Pro Arg Gly Arg Thr Phe Thr  
 195 200 205

Leu Lys Leu Thr Glu Pro Arg Lys Ala Phe Asp Met Ile Ser Gln Arg  
 210 215 220

Ser Ala Gly Gly Arg Pro Gly Ser Gly Pro Gln Leu Gly Thr Gly Arg  
 225 230 235 240

Gly Thr Leu Arg Leu Arg Ser Arg Gly Pro Ala Thr Val Glu Asp Leu  
 245 250 255

Pro Ser Ala Phe Glu Glu Lys Ala Ile Glu Lys Val Asp Asp Leu Leu  
 260 265 270

Glu Ser Tyr Met Gly Ile Arg Asp Thr Glu Leu Ala Ala Thr Met Val  
 275 280 285

Glu Leu Gly Lys Asp Lys Arg Asn Pro Asp Glu Leu Ala Glu Ala Leu  
 290 295 300

Asp Glu Arg Leu Gly Asp Phe Ala Phe Pro Asp Glu Phe Val Phe Asp  
 305 310 315 320

Val Trp Gly Ala Ile Gly Asp Ala Lys Val Gly Arg Tyr  
 325 330

<210> 15

<211> 1318

<212> DNA

<213> Human

<220>

B1  
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<221> misc\_feature

<222> (23)..(23)

<223> Where n = unknown

<220>

<221> misc\_feature

<222> (42)..(42)

<223> Where n = unknown

<220>

<221> misc\_feature

<222> (48)..(48)

<223> Where n = unknown

<220>

<221> misc\_feature

<222> (1105)..(1105)

<223> Where n = unknown

<400> 15

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ccagcaactc aaattcacca cctcggactc ctgcgaccgc atcaaagacg aatttcagct 180  
actgcaagct cagtaccaca gcctcaagct cgaatgtgac aagttggcca gtgagaagtc 240  
agagatgcag cgtcactatg tgatgtacta cgagatgtcc tacggcttga acatcgagat 300  
gcacaaacag gctgagatcg tcaaaaggct gaacgggatt tgtgcccagg tcctgcccta 360  
cctctcccaa gagcaccagc agcaggtcct gggagccatt gagagggcca agcaggtcac 420  
cgctcccgag ctgaactcta tcatccgaca gcagctccaa gccaccagc tgtccagct 480  
gcaggccctg gccctgccct tgaccccact acccggggg ctgcagccgc cttcgctgcc 540



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 cccatagtat ttatggtggc cgccggcggg ggcgccagcc cagcttgag gccacctcta 840  
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 gtaaccgaca gtctgcctgg gccacagccc tctcaacctg gtactgcatg cagcaatgc 1080  
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<210> 16

<211> 196

<212> PRT

<213> Human

<400> 16

Met Phe Pro Gln Ser Arg His Ser Gly Ser Ser His Leu Pro Gln Gln  
 1 5 10 15

Leu Lys Phe Thr Thr Ser Asp Ser Cys Asp Arg Ile Lys Asp Glu Phe  
 20 25 30

Gln Leu Leu Gln Ala Gln Tyr His Ser Leu Lys Leu Glu Cys Asp Lys  
 35 40 45

Leu Ala Ser Glu Lys Ser Glu Met Gln Arg His Tyr Val Met Tyr Tyr  
 50 55 60

Glu Met Ser Tyr Gly Leu Asn Ile Glu Met His Lys Gln Ala Glu Ile  
 65 70 75 80

B1  
Cont

Val Lys Arg Leu Asn Gly Ile Cys Ala Gln Val Leu Pro Tyr Leu Ser  
85 90 95

Gln Glu His Gln Gln Gln Val Leu Gly Ala Ile Glu Arg Ala Lys Gln  
100 105 110

Val Thr Ala Pro Glu Leu Asn Ser Ile Ile Arg Gln Gln Leu Gln Ala  
115 120 125

His Gln Leu Ser Gln Leu Gln Ala Leu Ala Leu Pro Leu Thr Pro Leu  
130 135 140

Pro Val Gly Leu Gln Pro Pro Ser Leu Pro Ala Val Ser Ala Gly Thr  
145 150 155 160

Gly Leu Leu Ser Leu Ser Ala Leu Gly Ser Gln Ala His Leu Ser Lys  
165 170 175

Glu Asp Lys Asn Gly His Asp Gly Asp Thr His Gln Glu Asp Asp Gly  
180 185 190

Glu Lys Ser Asp  
195

<210> 17

<211> 1264

<212> DNA

<213> Human

<220>

<221> misc\_feature

<222> (23)..(23)

<223> Where n = unknown

<220>

<221> misc\_feature

31  
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<222> (42) .. (42)

<223> Where n = unknown

<400> 17

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ccagcaactc aaattcacca cctcggactc ctgcgaccgc atcaaagacg aatttcagct 180  
actgcaagct cagtaccaca gcctcaagct cgaatgtgac aagttggcca gtgagaagtc 240  
agagatgcag cgtcactatg tgatgtacta cgagatgtcc tacggcttga acatcgagat 300  
gcacaaacag gctgagatcg tcaaaaggct gaacgggatt tgtgcccagg tctgccccta 360  
cctctcccaa gagcaccagc agcaggctctt gggagccatt gagagggcca agcaggctac 420  
cgctcccgag ctgaactcta tcatccgaca gcagctccaa gcccaccagc tgtcccagct 480  
gcaggccctg gccctgcctt tgacccact acccgtgggg ctgcagccgc cttcgtgcc 540  
ggcggtcagc gcaggcaccg gcctcctctc gctgtccgcg ctgggttccc aggccacct 600  
ctccaaggaa gacaagaacg ggcacgatgg tgaccccac caggaggatg atggcgagaa 660  
gtcggattag cagggggccg ggacaggag gttgggagg gggacagagg ggagacagag 720  
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gagcagggtg aggggtggcg acccaggatt cccctcccc ttcccaaata aagatgaggg 1260  
tact 1264

<210> 18

<211> 197

<212> PRT

<213> Human

<400> 18

Met Met Phe Pro Gln Ser Arg His Ser Gly Ser Ser His Leu Pro Gln  
1 5 10 15

Gln Leu Lys Phe Thr Thr Ser Asp Ser Cys Asp Arg Ile Lys Asp Glu  
20 25 30

Phe Gln Leu Leu Gln Ala Gln Tyr His Ser Leu Lys Leu Glu Cys Asp  
35 40 45

Lys Leu Ala Ser Glu Lys Ser Glu Met Gln Arg His Tyr Val Met Tyr  
50 55 60

Tyr Glu Met Ser Tyr Gly Leu Asn Ile Glu Met His Lys Gln Ala Glu  
65 70 75 80

Ile Val Lys Arg Leu Asn Gly Ile Cys Ala Gln Val Leu Pro Tyr Leu  
85 90 95

Ser Gln Glu His Gln Gln Gln Val Leu Gly Ala Ile Glu Arg Ala Lys  
100 105 110

Gln Val Thr Ala Pro Glu Leu Asn Ser Ile Ile Arg Gln Gln Leu Gln  
115 120 125

Ala His Gln Leu Ser Gln Leu Gln Ala Leu Ala Leu Pro Leu Thr Pro  
130 135 140

Leu Pro Val Gly Leu Gln Pro Pro Ser Leu Pro Ala Val Ser Ala Gly  
145 150 155 160

Thr Gly Leu Leu Ser Leu Ser Ala Leu Gly Ser Gln Ala His Leu Ser  
165 170 175

Lys Glu Asp Lys Asn Gly His Asp Gly Asp Thr His Gln Glu Asp Asp  
180 185 190

Gly Glu Lys Ser Asp  
195

<210> 19

<211> 1809

<212> DNA

<213> Human

<400> 19

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aacgagggcg tgtataatgg aagctgggga ggccggggag aggttattac gacctattgc 180  
cccgctaaca acgagccaat agcaagagtc cgacaggcca gtgtggcaga ctatgaagaa 240  
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gtaaaacagg gactttcaag tagcatcttt accaaagatc tgggcagaat ctttcgctgg 1380

B1  
Cont.

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 gatgcctgga aacagtacat gagaaggctt acttgacta tcaactacag taaagacctt 1560  
 cctctggccc aaggaatcaa gtttcagtaa aggtgtttta gatgaacatc ccttaatttg 1620  
 aggtgttcca gcagctgttt ttggagaaga caaagaagat taaagttttc cctgaataaa 1680  
 tgcattatta tgactgtgac agtgactaat cccctatga ccccaaagcc ctgattaaat 1740  
 caagagattc cttttttaa aatcaaaaata aaattgttac aacatagcca tagttactaa 1800  
 aaaaaaaaaa 1809

<210> 20

<211> 511

<212> PRT

<213> Human

<400> 20

Met Ser Thr Leu Leu Ile Asn Gln Pro Gln Tyr Ala Trp Leu Lys Glu  
 1 5 10 15

Leu Gly Leu Arg Glu Glu Asn Glu Gly Val Tyr Asn Gly Ser Trp Gly  
 20 25 30

Gly Arg Gly Glu Val Ile Thr Thr Tyr Cys Pro Ala Asn Asn Glu Pro  
 35 40 45

Ile Ala Arg Val Arg Gln Ala Ser Val Ala Asp Tyr Glu Glu Thr Val  
 50 55 60

Lys Lys Ala Arg Glu Ala Trp Lys Ile Trp Ala Asp Ile Pro Ala Pro  
 65 70 75 80

Lys Arg Gly Glu Ile Val Arg Gln Ile Gly Asp Ala Leu Arg Glu Lys  
 85 90 95

Ile Gln Val Leu Gly Ser Leu Val Ser Leu Glu Met Gly Lys Ile Leu  
 100 105 110

Val Glu Gly Val Gly Glu Val Gln Glu Tyr Val Asp Ile Cys Asp Tyr  
115 120 125

Ala Val Gly Leu Ser Arg Met Ile Gly Gly Pro Ile Leu Pro Ser Glu  
130 135 140

Arg Ser Gly His Ala Leu Ile Glu Gln Trp Asn Pro Val Gly Leu Val  
145 150 155 160

Gly Ile Ile Thr Ala Phe Asn Phe Pro Val Ala Val Tyr Gly Trp Asn  
165 170 175

Asn Ala Ile Ala Met Ile Cys Gly Asn Val Cys Leu Trp Lys Gly Ala  
180 185 190

Pro Thr Thr Ser Leu Ile Ser Val Ala Val Thr Lys Ile Ile Ala Lys  
195 200 205

Val Leu Glu Asp Asn Lys Leu Pro Gly Ala Ile Cys Ser Leu Thr Cys  
210 215 220

Gly Gly Ala Asp Ile Gly Thr Ala Met Ala Lys Asp Glu Arg Val Asn  
225 230 235 240

Leu Leu Ser Phe Thr Gly Ser Thr Gln Val Gly Lys Gln Val Gly Leu  
245 250 255

Met Val Gln Glu Arg Phe Gly Arg Ser Leu Leu Glu Leu Gly Gly Asn  
260 265 270

Asn Ala Ile Ile Ala Phe Glu Asp Ala Asp Leu Ser Leu Val Val Pro  
275 280 285

Ser Ala Leu Phe Ala Ala Val Gly Thr Ala Gly Gln Arg Cys Thr Thr  
290 295 300

Ala Arg Arg Leu Phe Ile His Glu Ser Ile His Asp Glu Val Val Asn  
305 310 315 320

Arg Leu Lys Lys Ala Tyr Ala Gln Ile Arg Val Gly Asn Pro Trp Asp  
325 330 335

Pro Asn Val Leu Tyr Gly Pro Leu His Thr Lys Gln Ala Val Ser Met  
340 345 350

Phe Leu Gly Ala Val Glu Glu Ala Lys Lys Glu Gly Gly Thr Val Val  
 355 360 365

Tyr Gly Gly Lys Val Met Asp Arg Pro Gly Asn Tyr Val Glu Pro Thr  
 370 375 380

Ile Val Thr Gly Leu Gly His Asp Ala Ser Ile Ala His Thr Glu Thr  
 385 390 395 400

Phe Ala Pro Ile Leu Tyr Val Phe Lys Phe Lys Asn Glu Glu Glu Val  
 405 410 415

Phe Ala Trp Asn Asn Glu Val Lys Gln Gly Leu Ser Ser Ser Ile Phe  
 420 425 430

Thr Lys Asp Leu Gly Arg Ile Phe Arg Trp Leu Gly Pro Lys Gly Ser  
 435 440 445

Asp Cys Gly Ile Val Asn Val Asn Ile Pro Thr Ser Gly Ala Glu Ile  
 450 455 460

Gly Gly Ala Phe Gly Gly Glu Lys His Thr Gly Gly Gly Arg Glu Ser  
 465 470 475 480

Gly Ser Asp Ala Trp Lys Gln Tyr Met Arg Arg Ser Thr Cys Thr Ile  
 485 490 495

Asn Tyr Ser Lys Asp Leu Pro Leu Ala Gln Gly Ile Lys Phe Gln  
 500 505 510

<210> 21

<211> 1428

<212> DNA

<213> Human

<400> 21

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acgcctggaa caaggaccgc acccagattg ccatctgccc caacaaccat gaggtgcata 180

B1  
cont



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gcaacgccta cgtgtggacg ctgaagggcc gcacatggaa gcccacgctg gtcacacctgc	360
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tgatgttcga atccagcagt agctgcggct ggggtacatgg cgtctgtttc tcagccagcg	720
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gcacggctgc gggcgcgggc ctagactcgc tgcacaagaa cagcgtcagc cagatctcgg	1080
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ggctaattggt tgctttgctg aatgtttctg gggtagcaat acgagttccc ataggggctg	1320
ctccctcaaa aaggaggagg acagatgggg agcttttctt acctattcaa ggaatacgtg	1380
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<210> 22

<211> 372

<212> PRT

<213> Human

<400> 22

Met	Ala	Tyr	His	Ser	Phe	Leu	Val	Glu	Pro	Ile	Ser	Cys	His	Ala	Trp
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Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val  
 20 25 30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu  
 35 40 45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser  
 50 55 60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr  
 65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn  
 85 90 95

Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala  
 100 105 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu  
 115 120 125

Asn Asp Trp Trp Val Cys Lys His Ile Lys Lys Pro Ile Arg Ser Thr  
 130 135 140

Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly  
 145 150 155 160

Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val  
 165 170 175

Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly  
 180 185 190

Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val  
 195 200 205

Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp, Ser  
 210 215 220

Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu  
 225 230 235 240

Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn  
 245 250 255

B1  
 Cont.

Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr  
 260 265 270

Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro  
 275 280 285

Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn  
 290 295 300

Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly  
 305 310 315 320

Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser  
 325 330 335

Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly  
 340 345 350

Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp  
 355 360 365

Leu Lys Ile Lys  
 370

<210> 23

<211> 1373

<212> DNA

<213> Human

<400> 23  
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 caggaagtac ttcgagggct tcggcgacat cgaggaggcc gtggatcatca cgcaccgcca 180  
 gacgggcaag tcccgcggct acggcttcgt gaccatggcc gaccgggcgg cagctgagag 240  
 ggcttgcaaa gaccctaacc ccatcatcga cggccgcaag gccaacgtga acctggcata 300  
 tctggggcgcc aagccttgggt gtctccagac gggcctttgcc attggcgtgc agcagctgca 360  
 cccaccttg atccagcgga cttacgggct gaccccgcac tacatctacc caccagccat 420

B1  
 cont.

cgtgcagcca gcgtggtgat cccagccgcc cctgtcccgt cgctgtcttc gccctacatt 480  
 gagtacacgc cggccagccc ggtctacgcc cagtaccac cggccaccta tgaccgtacc 540  
 catacgcgcg ctcgcctgcc acggctgaca gcttcgtggg ctacagctac cctgccgccg 600  
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 agcactgaag ttgcaacttt tttcttgtaa ttgttttgct actaagataa tttcagaagt 1320  
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<210> 24

<211> 230

<212> PRT

<213> Human

<400> 24

Ser Ala Gly Phe Ser Arg Pro Leu Ala Ala Pro Gly Val Met Tyr Gly  
 1 5 10 15

Ser Gln Lys Gly Thr Thr Phe Thr Lys Ile Phe Val Gly Gly Leu Pro  
 20 25 30

Tyr His Thr Thr Asp Ala Ser Leu Arg Lys Tyr Phe Glu Gly Phe Gly  
 35 40 45

Asp Ile Glu Glu Ala Val Val Ile Thr Asp Arg Gln Thr Gly Lys Ser  
50 55 60

Arg Gly Tyr Gly Phe Val Thr Met Ala Asp Arg Ala Ala Ala Glu Arg  
65 70 75 80

Ala Cys Lys Asp Pro Asn Pro Ile Ile Asp Gly Arg Lys Ala Asn Val  
85 90 95

Asn Leu Ala Tyr Leu Gly Ala Lys Pro Trp Cys Leu Gln Thr Gly Phe  
100 105 110

Ala Ile Gly Val Gln Gln Leu His Pro Thr Leu Ile Gln Arg Thr Tyr  
115 120 125

Gly Leu Thr Pro His Tyr Ile Tyr Pro Pro Ala Ile Val Gln Pro Ser  
130 135 140

Val Val Ile Pro Ala Ala Ala Pro Val Pro Ser Leu Ser Ser Pro Tyr  
145 150 155 160

Ile Glu Tyr Thr Pro Ala Ser Pro Val Tyr Ala Gln Tyr Pro Pro Ala  
165 170 175

Thr Tyr Asp Gln Tyr Pro Tyr Ala Ala Ser Pro Ala Thr Ala Asp Ser  
180 185 190

Phe Val Gly Tyr Ser Tyr Pro Ala Ala Val His Gln Ala Leu Ser Ala  
195 200 205

Ala Ala Pro Ala Gly Thr Thr Phe Val Gln Tyr Gln Ala Pro Gln Leu  
210 215 220

Gln Pro Asp Arg Met Gln  
225 230

<210> 25

<211> 1439

<212> DNA

<213> Human

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 gctcaggaag tacttcgagg gcttcggcga catcgaggag gccgtgggtca tcaccgaccg 180  
 ccagacgggc aagtcccgcg gctacggctt cgtgaccatg gccgaccggg cggcagctga 240  
 gagggcttgc aaagaccctt aaccccatca tcgacggccg caaggccaac gtgaacctgg 300  
 catatctggg cgccaagcct tgggtgtctc agacgggctt tgccattggc gtgcagcagc 360  
 tgcacccac cttgatccag cggacttacg ggctgacccc gcactacatc taccaccag 420  
 ccatcgtgca gccagcgtg gtgateccag ccgccctgt cccgtcgtg tctcgcct 480  
 acattgagta cagccggcc agcccgtct acgccagta cccaccggcc acctatgacc 540  
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 ccgccgtgca ccaggccctc tcagccgcag caccgcggg caccacttct gtgcagtacc 660  
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<210> 26

<211> 230

<212> PRT

<213> Human

B1  
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<400> 26

Arg Arg Met Gln Tyr Asn Arg Arg Phe Val Asn Val Val Pro Thr Phe  
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Gly Lys Lys Lys Gly Thr Thr Phe Thr Lys Ile Phe Val Gly Gly Leu  
20 25 30

Pro Tyr His Thr Thr Asp Ala Ser Leu Arg Lys Tyr Phe Glu Gly Phe  
35 40 45

Gly Asp Ile Glu Glu Ala Val Val Ile Thr Asp Arg Gln Thr Gly Lys  
50 55 60

Ser Arg Gly Tyr Gly Phe Val Thr Met Ala Asp Arg Ala Ala Ala Glu  
65 70 75 80

Arg Ala Cys Lys Asp Pro Asn Pro Ile Ile Asp Gly Arg Lys Ala Asn  
85 90 95

Val Asn Leu Ala Tyr Leu Gly Ala Lys Pro Trp Cys Leu Gln Thr Gly  
100 105 110

Phe Ala Ile Gly Val Gln Gln Leu His Pro Thr Leu Ile Gln Arg Thr  
115 120 125

Tyr Gly Leu Thr Pro His Tyr Ile Tyr Pro Pro Ala Ile Val Gln Pro  
130 135 140

Ser Val Val Ile Pro Ala Ala Pro Val Pro Ser Leu Ser Ser Pro Tyr  
145 150 155 160

Ile Glu Tyr Thr Pro Ala Ser Pro Val Tyr Ala Gln Tyr Pro Pro Ala  
165 170 175

Thr Tyr Asp Gln Tyr Pro Tyr Ala Ala Ser Pro Ala Thr Ala Asp Ser  
180 185 190

Phe Val Gly Tyr Ser Tyr Pro Ala Ala Val His Gln Ala Leu Ser Ala  
195 200 205

Ala Ala Pro Ala Gly Thr Thr Phe Val Gln Tyr Gln Ala Pro Gln Leu  
 210 215 220

Gln Pro Asp Arg Met Gln  
 225 230

<210> 27

<211> 2029

<212> DNA

<213> Human

<400> 27

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 agccgcgagg tgtccggcat caaggccgcc tacgaggccg agctcgggga tgcccgaag 480  
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 gaggagttaa aggagctgaa agcgcgcaat accaagaagg agggtagcct gatagctgct 600  
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 gctctcagtg agaagcgcac gctggagggc gagctgcagt atctgcgggg ccaggtggcc 720  
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 ctggacattg ccaggcagtc tgctgagagg aacagcaacc tgggtggggc tgcccacgag 1080  
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B1  
 Cont.



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cgggacacca gccggcggt gctggcgga aaggagcggg agatggccga gatggggca 1260  
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<210> 28

<211> 572

<212> PRT

<213> Human

<400> 28

Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala  
1 5 10 15

Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys  
20 25 30

Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg  
35 40 45

Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr  
50 55 60

Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala  
65 70 75 80

Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala  
85 90 95

Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu  
100 105 110

Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile  
115 120 125

Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys  
130 135 140

Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly  
145 150 155 160

Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu  
165 170 175

Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp  
180 185 190

Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys  
195 200 205

Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr  
210 215 220

Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg  
225 230 235 240

Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val  
245 250 255

Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp  
260 265 270

Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala  
275 280 285

His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala  
290 295 300

Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu  
305 310 315 320

Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg  
325 330 335

Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met  
340 345 350

Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala  
355 360 365

Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu  
370 375 380

Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly  
385 390 395 400

Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr  
405 410 415

Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln  
420 425 430

His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu  
435 440 445

Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met  
450 455 460

Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr  
465 470 475 480

Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr  
485 490 495

Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu  
500 505 510

Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr  
515 520 525

Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val  
530 535 540

Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp  
545 550 555 560

Leu Leu His His His His Val Ser Gly Ser Arg Arg  
565 570

B1  
Cont